

USSN 10/500,943

**LIST OF CLAIMS, SHOWING THE STATUS OF EACH CLAIM**

Underlining denotes added text while strikethrough denotes deleted text.

**IN THE CLAIMS:**

1. (Original) A protease variant of a precursor protease, said variant comprising one or more modifications at a charged amino acid residue position, said variant being characterized by having the same net electrostatic charge as said precursor protease.
2. (Original) The protease variant of claim 1, wherein said charged amino acid residue position is selected from the group consisting of aspartic acid, glutamic acid, lysine and arginine.
3. (Currently Amended) The protease variant of claim 1, wherein said variant comprises an amino acid sequence having a substitution at one or more residue positions equivalent to residue positions selected from the group consisting of 27, 45, 170, 181, 251 and 271 of *Bacillus amyloliquefaciens* subtilisin as set forth in SEQ ID NO. 2.
4. (Withdrawn) The protease variant of claim 3, wherein said variant comprises comprising a substitution at one or more positions corresponding to 27, 45, 170, 181, 251 and 271 is a substitution selected from K27T, R45N, R170S, D181N, K251G and E271T.
5. (Currently Amended) The protease variant of claim 3, further comprising an additional substitution at one or more positions corresponding to 1, 14, 49, 64, position 87, 100, 102, 118, 128, 204 and 258 of *Bacillus amyloliquefaciens* subtilisin as set forth in SEQ ID NO.2.

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6. (Withdrawn) The protease variant of claim 5, wherein variants are selected from the combinations of R45N-G118E-E271R, R45N-P14R, R45N-N204R, D181N-G118D, R45N-G258R, R170S-A1R, R170S-G61R, R170S-N204R, K251G-S87K, R170S-S216R, E271T-G100E, E271T-G102E, E271T-S128E, K27T-G100E, R170S-G100R, E271T-S49E and E271T-S128E.

7. (Original) A DNA encoding a protease variant of claim 2.
8. (Original) An expression vector encoding the DNA of claim 7.
9. (Original) A host cell transformed with the expression vector of claim 8.
10. (Original) A cleaning composition comprising the protease variant of claim 2.